

IM-5
SEQUENCE LISTING

<110> Wonderling, Ramani S.
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

<130> IM-5

<140> not yet assigned
<141> 2001-07-27

<150> 60/223,016
<151> 2000-08-04

<160> 109

<170> PatentIn version 3.1

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Xaa = unknown at position 119

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Met
1
act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164
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5 10 15
att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
20 25 30
aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
35 40 45
ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe
50 55 60 65

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gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa 356
 Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu
 70 75 80

ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta 404
 Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val
 85 90 95

acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac 452
 Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn
 100 105 110

aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat 500
 Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp
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gaa gga aat gac at 514
 Glu Gly Asn Asp
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 Xaa = unknown at position 119

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Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
 35 40 45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
 50 55 60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
 65 70 75 80

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Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
85 90 95

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

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115 120 125

Asp Glu Gly Asn Asp
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cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180
gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240
acttggtcgt tcaagtttcg taagattgag agtttatggt caagcttgcc aaagtaatct 300
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cccacaaagt tgatgcaatc atctactggg atagcagtca tctttatccc tgtgctcaat 420
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<222> (126)..(126)

<223> n = unknown at position 126
Xaa = unknown at position 43

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Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150

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Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser
110 115 120

cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag 437
Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln
125 130 135

aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg 485
Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu
140 145 150

tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa 533
Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys
155 160 165 170

ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc 581
Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe
175 180 185

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190

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Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
35 40 45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
50 55 60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
65 70 75 80

Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
85 90 95

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Val	Thr	Ile	Ser	Val	Asn	Tyr	Lys	Thr	Met	Ser	Thr	Leu	Ser	Cys	Glu
			100					105					110		

Asn	Lys	Ile	Ile	Ser	Phe	Lys	Glu	Met	Ser	Pro	Pro	Glu	Ser	Ile	Asn
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	130					135					140				

Asp	Asp	Lys	Ile	Gln	Phe	Glu	Ser	Ser	Leu	Tyr	Lys	Gly	Tyr	Phe	Leu
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Ala	Cys	Glu	Lys	Glu	Lys	Asp	Leu	Phe	Lys	Leu	Ile	Leu	Lys	Lys	Lys
				165					170					175	

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 gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180
 gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240
 gaatttatca tatatatgta taaagatagc ctactagag gtctggcagt aaccatctct 300
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agaacttgg	cgttcaagtt	tcgtaagatt	gagagtttat	gttcaagctt	gccaaagtaa	480
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Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu			
115	120	125	
aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat			432
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn			
130	135	140	
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145	150	155	

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Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
 35 40 45

Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
 50 55 60

Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
 65 70 75 80

Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
 85 90 95

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
 100 105 110

Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
 115 120 125

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Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn

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150

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 gtcagaatca ggcatacctt caaacacagg ttgatctccc tgggttaatga agagaacttg 420
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 20 25 30
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45
 acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192
 Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
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 Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
 65 70 75 80
 acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga 288

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Ala	Ser	Val	Asn	Asn	Met	Pro	Gly	Pro	Ala	Glu	Pro	Glu	Glu	Ser	Val		
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gat	gct	ctc	aag	ctt	tgt	cct	cgt	gaa	aac	ttc	gtg	aaa	ctg	tgt	aaa	432	
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg	Glu	Asn	Phe	Val	Lys	Leu	Cys	Lys		
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145					150					155					160		
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Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser		
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tcg	gac	agc	aca	ttc	ctg	gtg	ttc	atg	tct	cat	ggc	atc	ctg	agt	gga	720	
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly		
225					230					235					240		
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Ile	Cys	Gly	Thr	Lys	Tyr	Ser	Ala	Glu	Gly	Asp	Pro	Asp	Val	Leu	Ala		
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Tyr	Asp	Thr	Ile	Phe	Gln	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Leu	Ser	Leu		
			260					265					270				
aag	gac	aag	ccc	aag	gtc	atc	atc	gtc	cag	gcc	tgc	aga	ggg	gaa	aat	864	
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Val	Gln	Ala	Cys	Arg	Gly	Glu	Asn		
		275					280					285					
ttg	ggg	gaa	ctg	ttg	atc	agt	gac	tct	cca	gcg	gcc	cca	atg	gac	agc	912	
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser		
		290				295					300						
act	tca	cag	atg	ggg	agc	agc	ctt	tca	cag	gtg	ggg	gac	aac	cta	gag	960	
Thr	Ser	Gln	Met	Gly	Ser	Ser	Leu	Ser	Gln	Val	Gly	Asp	Asn	Leu	Glu		
305					310					315					320		

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Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
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<222> (18)..(524)
<223>
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 160 165

526

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<400> 18

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Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
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 35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
 50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
 65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
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Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
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Arg Leu Ala Leu Ile Ile Cys Asn Thr
 165

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 gcatctacag attcttctgg ctacagccggc ccaggcatgt tattcacgct ggctggaaga 180
 ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240
 gagagcccca gcgtctctgc aaggtgggtg tcttctctcac agatgtgaca gataaagatc 300
 tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360
 acggtagcgt tttcacattt tactctctcc atctctcctt ggttcagcac gtttttctca 420
 aagagttcat ccagcaagcc gttgaccgtc cccatgcoga ctgagttgat gaactgcttc 480
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 1 5 10 15
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 Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp
 20 25 30
 gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc 143
 Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys
 35 40 45
 tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct 191
 Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser
 50 55 60
 ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc 239
 Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys

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65	70	75	
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Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys			
80	85	90	95
cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca			335
Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr			
	100	105	110
aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc			382
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn			
	115	120	
agtccagccc ttcttgacca acttggaata gtaccttagc tagcacaaca cactcattta			442
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35 40 45

Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu
50 55 60

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
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Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
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Tyr Phe Tyr Leu Phe Pro Gly Asn
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 ccatgattgc tatttttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180
 ttcaatgggtg ggcatctggg ctctaacatt tggtttttca aatgactggt gtaccttccg 240
 aaataacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagttgtgt 300
 aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360
 gaaagcgatg aagtccttct ccacgtggac cttgtaaaatg gcgtcgtcct ctaggttgtc 420
 acccacctgt gaaaggctgc taccatctg tgaagtgtg tccattgggg ccgctggaga 480
 gtcactgate aacagttccc 500

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 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45

[illegible]

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ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc 912
 Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
 290 295 300

act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag 960
 Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
 305 310 315 320

gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc 1008
 Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
 325 330 335

tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga 1056
 Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
 340 345 350

tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg 1104
 Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
 355 360 365

tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa 1152
 Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
 370 375 380

aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg 1200
 Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
 385 390 395 400

aca aga tac ttc tat ctc ttc cct ggc aat 1230
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 405 410

<210> 24

<211> 410

<212> PRT

<213> Felis catus

<400> 24

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Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
 50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
 65 70 75 80

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Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
 165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
 180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
 195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
 210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
 225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
 245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
 260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
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Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
 290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu


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130	135	140	
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg			480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val			
145	150	155	160
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt			528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser			
165	170	175	
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac			576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp			
180	185	190	
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc			624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile			
195	200	205	
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca			672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro			
210	215	220	
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc			720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr			
225	230	235	240
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc			768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val			
245	250	255	
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag			816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys			
260	265	270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa			864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln			
275	280	285	
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg			912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val			
290	295	300	
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Ser Cys Ser			
305			
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<213> Felis catus			
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Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His

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	20	25	30
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	35	40	45
Ser Gly Lys	Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly		
	50	55	60
Gln Tyr Thr	Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu		
	65	70	75
Leu Ile His	Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg		
	85	90	95
Glu Gln Lys	Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys		
	100	105	110
Asn Tyr Ser	Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr		
	115	120	125
Asp Leu Lys	Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln		
	130	135	140
Glu Val Thr	Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val		
	145	150	155
Asp Asn Arg	Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser		
	165	170	175
Ala Cys Pro	Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp		
	180	185	190
Ala Ile His	Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile		
	195	200	205
Arg Asp Ile	Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro		
	210	215	220
Leu Lys Asn	Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr		
	225	230	235
			240

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Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
 260 265 270

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Ser Cys Ser
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 gaagaagctg ctgggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360
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 actgattgcc gtcagccacc agcagggtgaa acgtccagaa taattctttg cctcacattt 600
 tagaaagatc ttatTTTTTgg attctttctg ttcccttaag atatcagtgg accaaattcc 660
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 taggacttca ctgctctggg cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840
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 1 5 10 15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192
 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt 288
 Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg 336
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt 384
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg 432
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga 480
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160

ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca 528
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175

gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg 576
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190

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 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 195 200 205
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 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag 720
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc 768
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta 816
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac 864
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285
 aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat 912
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
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 gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
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 agc aac tgg gca tcc gtg tcc tgc agt 987
 Ser Asn Trp Ala Ser Val Ser Cys Ser
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<213> Felis catus

<400> 30

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 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

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295

300

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 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser
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 tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180
 gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcaactcca catgccgaga 240
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 gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360
 aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcttgacact ccactgtgta 420
 cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480
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 tagaaagatc ttattttttg attctttctg ttcccttaag atatcagtgg accaaattcc 660
 atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca 720
 ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780
 taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840
 ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900
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 ggcatgacc aactgctgag gatgcat 987

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 <211> 666
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS

<223>

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210

215

220

<210> 33
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 <212> PRT
 <213> Felis catus

<400> 33

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
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 20 25 30

Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
 35 40 45

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
 100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
 165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg

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205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
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 Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
 20 25 30
 gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat 144

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Pro	Leu	Glu	Leu	Thr	Met	Asn	Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile		
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Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe		
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Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr		
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Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys		
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Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu		
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Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu		
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ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	576	
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser		
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Tyr	Leu	Asn	Ala	Ser													
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<213> Felis catus

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			20					25					30		

IM-5

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
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Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
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Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
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Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
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Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
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Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
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ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctgggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

Year	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val 180 185 190	576
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
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His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu			
385	390	395	400
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc			1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile			
	405	410	415
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt			1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe			
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atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac			1344
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr			
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cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa			1392
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys			
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agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg			1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu			
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35

40

45

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100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
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Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
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Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
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Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
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IM-5

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Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
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Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
 485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
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IM-5

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Tyr Leu Asn Ala Ser
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Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln	
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IM-5

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Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
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Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
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Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
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Page 53

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Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu					
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Ala	Arg	Gln 35	Thr	Leu	Glu	Leu	Tyr 40	Ser	Cys	Thr	Ser	Glu 45	Glu	Ile	Asp
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Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys	
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Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln	
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Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
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Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
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 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
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 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctg 144
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
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 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
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 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys

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IM-5

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985

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 <213> Felis catus

<400> 56

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Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
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Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
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Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
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Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
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Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
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Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
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Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
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Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
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Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
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IM-5

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
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Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
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Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
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Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
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Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
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Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
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Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
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IM-5

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 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
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gcc Ala	aag Lys	atc Ile	cgc Arg	gtg Val	caa Gln	gcc Ala	cga Arg	gac Asp	cgc Arg	tac Tyr	tat Tyr	agt Ser	tca Ser	tcc Ser	tgg Trp	960
310315320																
agc Ser	gac Asp	tgg Trp	gca Ala	tct Ser	gtg Val	tca Ser	tgc Cys	agt Ser	ggg Gly	ggc Gly	ggg Gly	ggc Gly	ggc Gly	gga Gly	tct Ser	1008
325330335																
aga Arg	aac Asn	ttg Leu	cca Pro	acc Thr	cct Pro	act Thr	cca Pro	tcc Ser	ccg Pro	ggg Gly	atg Met	ttc Phe	caa Gln	tgt Cys	ttg Leu	1056
340345350																
aac Asn	cac His	tcc Ser	caa Gln	acc Thr	ttg Leu	ttg Leu	aga Arg	gcc Ala	gtc Val	agc Ser	aac Asn	acg Thr	ctt Leu	cag Gln	aag Lys	1104
355360365																

IM-5

gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 1152
 Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 370 375 380

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta 1200
 His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 385 390 395 400

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc 1248
 Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 405 410 415

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt 1296
 Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
 420 425 430

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac 1344
 Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 435 440 445

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag 1392
 Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 450 455 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg 1440
 Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 465 470 475 480

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc 1488
 Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
 485 490 495

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 1536
 Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 500 505 510

ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc 1584
 Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
 515 520 525

tac ttg aac tct tcc 1599
 Tyr Leu Asn Ser Ser
 530

<210> 62
 <211> 533
 <212> PRT
 <213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
 20 25 30

IM-5

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

00012466-02204

260

265

270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
 355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
 420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
 485 490 495

IM-5

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ser Ser
530

<210> 63
<211> 1599
<212> DNA
<213> Canis familiaris

<400> 63
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ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatgggtta ttccagtggg aagcaggcct ccactgtgct 420
ggtttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccgggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780
tgtcagggag aagtaggaat gtgggggtgct ccaggtgtcg gggatttccc agctgacctc 840
cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctggtgta gttttcatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatgggta ggctctctc ggagagggg caggcactgc cctoctgaca 1020
ctccactgtg tactttctat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080
cactgctcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaataca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200
tgccacacat ttcagaaaga tcttattttt ggattctttt tgttccttta agatatcagt 1260

IM-5

ggaccaaatt ccattcttctt ttttgtgaat caacaggagt gagcgggtca gaaccttgcc 1320
 tccttttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380
 tttaccagaa ctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
 tacaacataa acatctttct ccagttccca tatggccatg aggggagacg ccagcaaac 1560
 gagggaaaac caggagatga ccaactgctg aggggtgcat 1599

<210> 64
 <211> 0
 <212> DNA
 <213> Canis familiaris

<400> 64
 000

<210> 65
 <211> 0
 <212> DNA
 <213> Canis familiaris

<400> 65
 000

<210> 66
 <211> 1533
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(1533)
 <223>

<400> 66
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 Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
 1 5 10 15
 cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa 96
 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
 20 25 30
 gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144
 Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
 35 40 45
 tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192
 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60
 cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240

IM-5

Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val	Leu	Ser	Arg	Ser	Leu	Leu		
65					70					75					80		
ttg	att	cac	aaa	aaa	gaa	gat	gga	att	tgg	tcc	act	gat	atc	tta	aag	288	
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Lys		
				85					90					95			
gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	ctg	aaa	tgt	gag	gca	aag	336	
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys		
			100					105					110				
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384	
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr		
		115					120					125					
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432	
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln		
	130					135					140						
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480	
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val		
145					150					155					160		
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528	
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser		
				165					170					175			
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576	
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp		
			180					185					190				
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624	
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile		
		195					200					205					
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672	
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro		
	210					215					220						
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720	
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr		
225					230					235				240			
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala		
				245					250					255			
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816	
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys		
			260					265					270				
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864	
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln		
		275					280					285					
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912	
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val		
	290					295					300						

IM-5

Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

IM-5

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
325 330 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
340 345 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385 390 395 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465 IM-5 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
500 505 510

<210> 68
<211> 1533
<212> DNA
<213> Canis familiaris

<400> 68
ggaagagttc aagtaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg 60
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ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct cactgtgct 420
ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca cactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
gtccacgcag agtctatctt tcttttctct attgttcttg ccttgggcct gtatgcaaaa 780
tgtcaggag aagtaggaat gtgggggtgct ccagggtgtc gggatttccc agctgacctc 840
cacgtgccga gaatttttca atggcctcag ctgcaggttt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctggtgta gtttccatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatgggta ggctctctc ggagagggg caggcactgc cctcctgaca 1020
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cactgtcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaataca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200
tgctcacat ttcagaaaga tcttattttt ggattcttct tgttccttta agatatcagt 1260

IM-5
ggaccaaatt ccattcttctt ttttgtgaat caacaggagt gagcgggtca gaaccttgcc 1320
tcctttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380
tttaccagaa ctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440
aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
tacaacataa acattcttctt ccagttccca tat 1533

<210> 69
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 69
gccaagctcg aaattaaccc tcactaaagg 30

<210> 70
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 70
cgacggccag tgaattgtaa tacgactc 28

<210> 71
<211> 31
<212> DNA
<213> Artificial sequence

<220>
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<400> 71
agtgatgaag gcctggaatc agattacttt g 31

<210> 72
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 72
atggcctgga acattctctt gaaagaatat ga 32

<210> 73
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 73
 aactattgag cacagggata aagatgactg 30

 <210> 74
 <211> 33
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 74
 aatatctaatt tcttggttttg aacagtgaac att 33

 <210> 75
 <211> 36
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 75
 tatgccggct actttggcaa gcttgaacat aaactc 36

 <210> 76
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 76
 ggccctcgagc taattcttgt tttgaacagt gaacatt 37

 <210> 77
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 77
 atggccgaca aggtcctgaa ggagaaga 28

<210> 78
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 78
 ttaatgtcct gggaagaggt agaaacatct tgt 33

<210> 79
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 79
 tcaagccac aatctggaaa ttctca 26

<210> 80
 <211> 26
 <212> DNA
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<220>
 <223> Synthetic Primer

<400> 80
 ctggagagtc actgatcaac agttcc 26

<210> 81
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 81
 acaaggatcc accatggccg acaaggatct gaaggg 36

<210> 82
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 82
 cgctctaga cctcaattgc cagggaagag atagaagta 39

<210> 83
 <211> 60
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 83
 ctgcagtggg ggcggtggcg gcggatctag aaacttgcca acccctactc catccccggg 60

<210> 84
 <211> 60
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 84
 cccgggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgcc accactgcag 60

<210> 85
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 85
 atgcatcctc agcagttggt catcgcct 28

<210> 86
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 86
 tgcaggacac ggatgcccag ttgct 25

<210> 87
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 87

IM-5
acaggtacca tgcatacctca gcagttggtc atcgctt 37

<210> 88
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 88
ctaactgcag gacacggatg cccag 25

<210> 89
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 89
atgtgcccgc cgcgtggcc 19

<210> 90
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 90
ctaggaagca ttcagatagc tcatcat 27

<210> 91
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 91
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<210> 92
<211> 41
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<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 92
atgactgcgg ccgcctagga agcattcaga tagctcatca t 41

<210> 93
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 93
ccatcctggg cctgctaagc 20

<210> 94
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 94
ccatctggta catcttcaag tc 22

<210> 95
<211> 38
<212> DNA
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<220>
<223> Synthetic Primer

<400> 95
aaaaaacccg ggtatgttcc aatgtttcaa ccaactccc 38

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<211> 51
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<220>
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<400> 96
gcggccgctc gagttaggaa gagttcaagt aggacatcat tctattgatg g 51

<210> 97
<211> 22
<212> DNA
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<220>
<223> Synthetic Primer

<400> 97
cttaaaggaa cagaaagaat cc 22

<210> 98
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 98
ggtattccca gctgacctc 19

<210> 99
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 99
cataggtacc atgcaccctc agcagttggt catctcc 37

<210> 100
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 100
atctaaatgc atgacacaga tgcccagtc 29

<210> 101
<211> 561
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(561)
<223>

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Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1 5 10 15

agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys

[illegible]

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<210> 102
<211> 187
<212> PRT
<213> Felis catus
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Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1 5 10 15

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser

35

40

45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
180 185

<210> 103

<211> 561

<212> DNA

<213> Felis catus

<400> 103

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggctgtaac agtcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct cactgtgtgt 420

IM-5

ggttttatct tttgtgatat cttcatgata aatctcttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540
gttgaggcac tggaacatcc c 561

<210> 104
<211> 1455
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (232)..(897)
<223>

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gccaattata aaaatgtgac cccccgggtc ggccctccac cgccgcccctc ccctgccgag 180
tccgcagtcc gcgtccagcg cccgccgggg tccacgcagc gcccgcagc c atg tgc 237
Met Cys
1
ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285
Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His
5 10 15
ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333
Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser
20 25 30
cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381
Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala
35 40 45 50
gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc 429
Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser
55 60 65
tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc 477
Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
70 75 80
agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt 525
Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser
85 90 95
tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg 573
Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu
100 105 110
gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc 621
Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile

IM-5

115	120	125	130	
tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca				669
Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala				
	135	140	145	
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg				717
Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met				
	150	155	160	
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg				765
Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val				
	165	170	175	
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act				813
Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr				
	180	185	190	
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg				861
Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val				
	195	200	210	
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg				907
Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser				
	215	220		
aggtctctct cgactttaaa gtcattccta taaaaatgtg aacccaaaag aatttttcat				967
aagatagggg ttaagaacca gggagggggg ggcttgacct ggtcctactt aagctagtag				1027
gataattctc atgcttggtt acattagttg ccactcaaat tttgaaagat gtgactgtta				1087
tatcccacac gatgcctttg accaagtata tttcacatit actatggata agttaagtgt				1147
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taatagaaga gcaagacttt ataagctatt tctgtaccaa actgttttga gaaacaaaca				1267
ctcaagcata atttatttta aaatacttat ttatataatt ttgtgttcat gaaagcatgt				1327
gaattaatit atatttattt atgttatatt tattaaagta tttattatca agtggatttg				1387
ggatatctta tgttctaaaa ataaaatgat tgagtagaaa aaaaaaaaaa aaaaaaaaaa				1447
aaaaaaaa				1455

<210> 105

<211> 222

<212> PRT

<213> Canis familiaris

<400> 105

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
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Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser

20

25

30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
 35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
 100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
 165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
 195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
 210 215 220

<210> 106

<211> 1455

<212> DNA

<213> Canis familiaris

<400> 106

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60

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 tgcttgagtg tttgtttcta caaacagttt ggtacagaaa tagcttataa agtcttgctc 240
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 gctcacgaac acttaactta tccatagtaa atgtgaaata tacttgggtca aaggcatcgt 360
 gtgggatata acagtcacat ctttcaaaat ttgagtggca actaatgtaa acaagcatga 420
 gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480
 cctatcttat gaaaaattct tttgggttca catttttata ggaatgactt taaagtcgag 540
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 acgaattctg aaagcatgaa gaagtatgca gagcttgatt ttagttttat aaaaatccgg 660
 ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720
 ctcatcgata gctgtcagca tgttttgatc cagaaagatc tgctctctgg gatccattaa 780
 aagctttgcg ttcattggcct tgaattccat ctggtacatc ttcaagtcct catagatgct 840
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 tatcaaagag atctctctgg aagccaggca actctcattc atggttaatt ccagtggtaa 960
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 ggtttgctc gtgcc 1455

<210> 107
 <211> 2267
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (154)..(1140)
 <223>

IM-5

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cccaggggaac cttgcagcct ggccagaagc aag atg cat cct cag cag ttg gtc 174
Met His Pro Gln Gln Leu Val
1 5
atc tcc tgg ttt tcc ctc gtt ttg ctg gcg tct ccc ctc atg gcc ata 222
Ile Ser Trp Phe Ser Leu Val Leu Leu Ala Ser Pro Leu Met Ala Ile
10 15 20
tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac cct 270
Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His Pro
25 30 35
gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa gaa 318
Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu Glu
40 45 50 55
gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt tct 366
Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly Ser
60 65 70
ggg aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc cag 414
Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln
75 80 85
tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg ttg 462
Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu Leu
90 95 100
att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag gaa 510
Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Glu
105 110 115
cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat 558
Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn
120 125 130 135
tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat 606
Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp
140 145 150
ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg 654
Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly
155 160 165
gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac 702
Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp
170 175 180
aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc 750
Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala
185 190 195
tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct 798

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Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	Ala		
200					205					210					215		
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Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	Arg		
				220					225					230			
gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	ttg	894	
Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	Leu		
			235					240					245				
aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	tgg	942	
Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	Trp		
		250						255				260					
agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	cag	990	
Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	Gln		
	265					270					275						
ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	acc	1038	
Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	Thr		
280					285					290					295		
tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	gcc	1086	
Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	Ala		
				300					305					310			
cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	tcc	1134	
Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	Ser		
			315					320					325				
tgc	agt	taggttccac	ccccaggatg	aatcttggag	ggaaagtgga	agatattatg										1190	
Cys	Ser																
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IM-5

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 tggtaagaa ttgcttactg gacagcgcaa gtgaacctga ctggtggatg tgaccagaaa 2090
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<210> 108
 <211> 329
 <212> PRT
 <213> Canis familiaris

<400> 108

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
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 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160

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Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
 225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser
 325

<210> 109

<211> 2267

<212> DNA

<213> Canis familiaris

<400> 109

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aatcacttta cagaaagcac attcattact taaaagtagc acctcagcga ttggcacttt 180

ctggtcacat ccaccagtca ggttcacttg cgctgtccag taagcaattc ttgaccattt 240

IM-5

tctttgcatc catgtgcttt ttttgccctgg ctattaagga gcagctggaa attctgacaa 300
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ccaccgcaag gaagtcttta tggatacagg atctaacatc tccgtctcca gaaacttctc 600
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